



SEQUENCE LISTING

<110> Swenson, David
Cepheid

<120> Controls for Primers in Multiplex Amplification
Reactions

<130> 020048-001710US

<140> US 10/721,579
<141> 2003-11-24

<150> US 60/429,834
<151> 2002-11-27

<160> 15

<170> PatentIn Ver. 2.1

<210> 1
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria A
specific PCR target sequence

<400> 1
ggtcggaag tgtaacgagg tggaaagcgc accatcgaaa ctattacaag tcccttgatg 60
gaagattatg tcgaccactt t 81

<210> 2
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:complementary
sequence to the target sequence for Bacteria A

<400> 2
aaagtggtcg acataatctt ccatcaaggg actagtaata gaaacgatgg tgcgtttcc 60
acctcggtac acttccgac c 81

<210> 3
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria A
forward primer

<400> 3
ttacacttcc gcacc

15

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<210> 4
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria A
      reverse primer

<400> 4
tatgtcgacc acttt                                         15

<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Beacons probe
      for Bacteria A

<220>
<221> modified_base
<222> (1)
<223> n = c modified by FAM

<220>
<221> modified_base
<222> (27)
<223> n = g modified by Dabcyl

<400> 5
ncacgcacta gtaatagaaa cgcgtgn                                         27

<210> 6
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria B
      specific PCR target sequence

<400> 6
gcacgcgtat gcagcgacga tgcagcgacg agtcgaggct aggcgagcag ctttatctat 60
catcgtgatc gtgtacgtag cttagcatctg                                         90

<210> 7
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:complementary
      sequence to the target sequence for Bacteria B

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<400> 7
cagatgctag ctacgtacac gatcacgatg atagataaaag ctgctcgctt agcctcgact 60
cgtcgctgca tcgtcgctgc atacgcgtgc 90

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria B
      forward primer

<400> 8
gctgcatacg cgtgc 15

<210> 9
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Bacteria B
      reverse primer, Target 2 reverse primer sequence

<400> 9
cgttagctagc atctg 15

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Beacons probe
      for Bacteria B

<220>
<221> modified_base
<222> (1)
<223> n = c modified by Texas Red

<220>
<221> modified_base
<222> (30)
<223> n = g modified by Dabcyl

<400> 10
ncacgcgtg ctcgccttagc ctcggcgtgn 30

<210> 11
<211> 111
<212> DNA
<213> Artificial Sequence

```

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<220>
<223> Description of Artificial Sequence:Internal
      Control Oligo

<400> 11
ggtgccggaaacgtgtaaaaacgttagcttagcataaaagcttagc atctgaaatc gagctgatgc 60
tgcaaagctgcatacgcgaa agcatacgcg tgcaaatacg tcgaccactt t           111

<210> 12
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:complementary
      sequence to the target sequence for Internal
      Control Oligo

<400> 12
aaagtggtcg acatatttgc acgcgtatgc tttcgctaa gcagcttgc agcatcagct 60
cgatttcaga tgctagctt tatgctagct acgttttac acttccgcac c           111

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Beacons probe
      for the Internal Control

<220>
<221> modified_base
<222> (1)
<223> n = c modified by TET

<220>
<221> modified_base
<222> (27)
<223> n = g modified by Dabcyl

<400> 13
ncacgcgcag catcagctcg agcgtgn                                         27

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Target 2
      reverse primer subsequences

<400> 14
cgttagctgc atctgaaaag ctagcatctg                                         30

```

```
<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Target 2
      reverse primer subsequences

<220>
<221> modified_base
<222> (10)..(21)
<223> n = g, a, c or t; unrelated nucleotides separating
      Target 2 reverse primer subsequences

<400> 15
cgtagctagn nnnnnnnnnn ncatctg
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